

GenCore version 5.1.5  
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OM nucleic - nucleic search, using sw model

Run on: June 1, 2003, 15:21:24 ; Search time 2494.08 seconds  
(without alignments)  
12850.800 Million cell updates/sec

Title: US-09-625-573-3  
Perfect score: 1979  
Sequence: 1 CAGGACTGCTGAGACAAGC.....ATATGCAATATAAAATTTAG 1979

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues  
Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

#### Database :

```

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	469.8	23.7	807	13	BI764263 603045953
2	469	23.7	469	17	B84215 RPT111-22K6
3	357.6	18.1	487	10	BE656336
4	326.2	16.5	542	9	AA547303 vk28h04.r
5	296.4	15.0	480	10	AW657263 109996 MA
6	292.6	14.8	447	9	AA671573 v104g01.r

7	289	14.6	1074	14	BM917063
8	284.8	14.4	452	9	AI851510
9	276.6	14.0	907	9	AL552677
10	249.8	12.6	789	12	BG205056
11	247.8	12.5	341	17	AQ066245
12	239.4	12.1	869	12	BF119225
13	236.4	11.9	876	13	BI906283
14	235.2	11.9	884	12	BG182330
15	230	11.6	230	12	BF171452
16	220.8	11.2	952	14	BM917763
17	216.8	11.0	745	12	BG204024
18	214.6	10.8	1167	14	BQ053936
19	198.6	10.0	650	10	BB630138
20	197	10.0	672	10	BB638766
21	196.2	9.9	568	12	BF193051
22	189	9.6	780	13	BI908127
23	186.8	9.4	551	12	BF081124
24	181	9.1	863	13	BI661279
25	180.6	9.1	669	13	BI393893
26	179.4	9.1	533	12	BF193021
27	177.2	8.9	639	10	BB629533
28	175.2	8.9	723	14	BM951933
29	173.6	8.8	965	14	BQ944555
30	172.2	8.7	934	12	BG460984
31	169.2	8.5	787	9	AU080004
32	168.8	8.5	3005	11	AK019478
33	163.8	8.3	936	12	BF119806
34	153.2	7.7	665	10	BB628567
35	151.8	7.7	682	10	BB644135
36	151.6	7.7	600	13	BI987229
37	151.6	7.7	646	10	BB615634
38	147.2	7.4	867	13	BI106339
39	146.4	7.4	2111	11	AK007808
40	145.4	7.3	319	14	BM734515
41	141.2	7.1	574	17	AQ461727
42	140.6	7.1	804	13	BI685810
43	139.6	7.1	427	12	BF081123
44	138.2	7.0	668	10	BB45326
45	138	7.0	770	9	AJ452673

#### ALIGNMENTS

```

RESULT 1
BI764263
LOCUS
DEFINITION 603045953F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5186388 5',
            807 bp mRNA linear EST 25-SEP-2001
ACCESSION BI764263
VERSION BI764263.1 GI:15755841
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 807)
            NIH-MGC http://mgs.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgaps-remail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            CDNA Library Prepared by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone Distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11465 row: i column: 13
            High quality sequence stop: 805.
FEATURES
            Location/Qualifiers
                source
                    1..807

```

```
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5186388"
/clone_lib="NIH_MGC_116"
/lab_host="DH10B"
/notes="Organ: pooled colon, kidney, stomach; Vector:
pcmv-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 3 colons, age 26 yo male, 49 yo
female, 71 yo male colon; 46 yo male kidney, and pool of 2
stomachs, 62 yo male and 70 yo female. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.4 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
023. Note: this is a NIH_MGC Library."
BASE COUNT      186 a 209 c 171 g 241 t
ORIGIN

Query Match      23.7%; Score 469.8; DB 13; Length 807;
Best Local Similarity 82.5%; Pred. No. 3e-120;
Matches 603; Conservative 0; Mismatches 112; Indels 16; Gaps 5;

QY 154 ATTATGATTACGGTGTCTCCCTGTCATAAATTGACGTGAGCAAAATGGGGCCCACTCC 213
      ||||| || ||||| || ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 81 ATTATGATTACGGTGTCTCCCTGTCATAAATTGACGTGAGCAAAATGGGGCCCACTCC 140
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 214 TGCCTCCGCTGTCACCTGCTGTTTCACTTTGTTTGGTGGCAACATGCTGCTGCTCC 273
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 141 TGCCTCCGCTGTCACCTGCTGTTTCACTTTGTTTGGTGGCAACATGCTGCTGCTCC 200
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 274 TCATCTTAATACGCAAAAGCTGAACTGCTGACTGACATTTACCTGCTCAACTGG 333
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 201 TCATCTTAATACGCAAAAGCTGAAAGCATGACTGACATCTACCTGCTCAACTGG 260
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 334 COATCTGATGCTGCTTTTCTTATTACTCTCCATTTGGTGGTCACTGCTGCAATG 393
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 261 COATCTGATGCTGCTTTTCTTATTACTCTCCATTTGGTGGTCACTGCTGCAATG 320
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 394 AGTGGGTCTTGGGAATGCAATGCGAATATTACAGGGCTGTATCATCTCGGTTAT 453
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 321 AGTGGGAC-TTGGAAATACATGTGTCAACTCTTGACAGGGCTCTATTATTATAGGCTTCT 379
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 454 TTGGCGGAATCTTCTTCATCATCTCTGACAAATCGATAGATACCTGGCTATGTCATG 513
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 380 TCTCTGGAATCTTCTTCATCATCTCTGACAAATCGATAGATACCTGGCTGCTGCTCATG 439
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 514 CTGTTGTTGCTTTAAAGCCAGGAGCGTACCTTTGGGTGGTGGCAAGTGTGATCACT 573
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 440 CTGTTGTTGCTTTAAAGCCAGGAGCGTACCTTTGGGTGGTGGCAAGTGTGATCACT 499
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 574 GTTGGTGGCTGTTGCTTCTGTCAGGAATCATCTTTACTAAATGCCAGAAAGAAG 633
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 500 GGGTGGTGGCTGTTGCTTCTGTCAGGAATCATCTTTACCAGATCTCAAAAGAAG 559
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 634 ATTCTGTTTATGCTGTGGCCCTTATTTTCCA-----CGAGATGGAATAAT 581
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 560 GTCTTCATTACCTGACCTCTCAATTTCCATACAGTCAGTATCAATTTCTGGAAGAAT 619
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 582 TCCACAAATATGAGGAACATTTTGGGCTGGTCTGCCGCTGCTCATCTGTTGCTATCT 741
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 620 TCCAGACATTAAGATAGTATCTGTTGGGCTGGTCTGCCGCTGCTTGTCTATGTTCACT 679
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 742 GCTACTCGGAATCTGAAACCTCTGTTGCGTTCGAAACGAGAAAGAGGCGATAGG 801
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 680 GCTACTCGGAATCTGAAACCTCTGTTGCGTTCGAAACGAGAAAGAGGCGACACA-GG 738
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 802 CAGTGAGAGTCACTTCAACCATCATGATTGTTTACTTCTCTCTGAGCTCCCTATAACA 861
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 739 CTGTGAGGCTTATCTTCAACCATCATGATTGTTTACTTCTCTCTGAGCTCCCTATAACA 861
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 862 TTGTCATCTC 872
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```

Db 797 TTGCTCTTCTC 807

RESULT 2

LOCUS B84215

DEFINITION RPC111-22K6-TV RPC1-11 Homo sapiens genomic clone RPC1-11-22K6, DNA sequence.

ACCESSION B84215

VERSION B84215.1 GI:2925347

KEYWORDS GSS.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 469)

AUTHORS Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and Venter,J.C.

TITLE Use of BAC End Sequences for Sequence-Ready Map Building (1998)

JOURNAL Unpublished (1998)

COMMENT Other\_GSSs: RPC111-22K6.tp

Contact: Mark Adams

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0208

Email: mdadams@tigr.org

Clones are derived from the human BAC library RPC1-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tldb/hungen/bac\_end\_search/bac\_end\_search.html

Seq primer: T7

Class: BAC end.

Location/Qualifiers

1. 469

/organism="Homo sapiens"

/db\_xref="GDB:7508309"

/db\_xref="taxon:9606"

/clone="RPC1-11-22K6"

/clone\_lib="RPC1-11"

/sex="Male"

/cell\_type="Lymphocytes"

/note="Vector: pBAC3.6; Site\_1: EcoRI; Site\_2: EcoRI; RPC111 Human Male BAC library"

BASE COUNT 141 a 103 c 113 g 112 t

ORIGIN

Query Match 23.7%; Score 469; DB 17; Length 469;

Best Local Similarity 100.0%; Pred. No. 4.2e-120;

Matches 469; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 894 TTCGGCTGAGTAACCTGAAAGCACCAGTCACTGGACCAAGCCAGCAGGTGACAGAG 953

Db 1 TTCGGCTGAGTAACCTGAAAGCACCAGTCACTGGACCAAGCCAGCAGGTGACAGAG 60

QY 954 ACTCTTGGGATGACTCACTGCTGCATCAATCCCATCATCTATGCTTGTGGGGAGAAG 1013

Db 61 ACTCTTGGGATGACTCACTGCTGCATCAATCCCATCATCTATGCTTGTGGGGAGAAG 120

QY 1014 TTCAGAAGGTATCTCTCGGTGTTCTTCCGAAAGCACATCACAAGCGCTTCTGCAACAA 1073

Db 121 TTCAGAAGGTATCTCTCGGTGTTCTTCCGAAAGCACATCACAAGCGCTTCTGCAACAA 180

QY 1074 TGTCCAGTTTCTACAGGGAGACAGTGGAGTGGAGTACTTCAACAAACACGCCCTTCCACT 1133

Db 181 TGTCCAGTTTCTACAGGGAGACAGTGGAGTGGAGTACTTCAACAAACACGCCCTTCCACT 240

QY 1134 GGGAGCAGGAAGTCTCGGCTGGTGTATTAACAGCAGCAGTGTGATTGTTGTTATAA 1193

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 241 GGGAGCAGGAAGTCTCGCTGGTTTATATAAAGAGGAGCAGCTTGAATTTGTTTATTA 300  
 QY 1194 AGGAGATAACAATCTGTATATAACAACAACAACTTCAAGGGTTTGTGTAACAATAGAAC 1253  
 Db 301 AGGAGATAACAATCTGTATATAACAACAACAACTTCAAGGGTTTGTGTAACAATAGAAC 360  
 QY 1254 TGTAAAGCAGGTGCCAGGAACCTCAGGCTGTGTGTACTATACAGACTATGTACCCA 1313  
 Db 361 TGTAAAGCAGGTGCCAGGAACCTCAGGCTGTGTGTACTATACAGACTATGTACCCA 420  
 QY 1314 ATGCATATCCACATGTCTCAGGAATAATCCAGAAAACCTGTGGTA 1362  
 Db 421 ATGCATATCCACATGTCTCAGGAATAATCCAGAAAACCTGTGGTA 469

RESULT 3  
 BE56336  
 LOCUS  
 DEFINITION UI-M-BH0-aju-h-06-0-UI.r1 NIH.BMAP\_M.S1 Mus musculus cDNA clone  
 UI-M-BH0-aju-h-06-0-UI 5', mRNA sequence.  
 ACCESSION BE56336  
 VERSION BE56336.1 GI:9982249  
 KEYWORDS EST.  
 SOURCE house mouse.  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 487)  
 Ronaldo,M.F., Lennon,G. and Soares,M.B.  
 Normalization and subtraction: two approaches to facilitate gene  
 discovery  
 Genome Res. 6 (9), 791-806 (1996)  
 9704477  
 Contact: Chin, H  
 National Institute of Mental Health  
 6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD  
 20892-9643, USA  
 Tel: 301 443 1706  
 Fax: 301 443 9890  
 Email: mestr@mail.nih.gov  
 CDNA Library Preparation: M.B. Soares Lab Clone Distribution:  
 Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS. It  
 should be noted that Bento Soares is generating a small number of  
 additional specialized non-redundant arrays of BMAP cDNAs whose  
 availability will be considered under appropriate and limited  
 collaborative arrangements  
 Seq primer: M13 Reverse.

FEATURES  
 Source  
 1. .487  
 /organism="Mus musculus"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone\_lib="NIH.BMAP\_M.S1"  
 /dev\_stage="27-32 days"  
 /lab\_host="DH10B (Life Technologies)"  
 /note="Vector: pT73D-Pac (Pharmacia) with a modified  
 polylinker; Site.1: Not I; Site.2: Eco RI; The  
 NIH.BMAP\_M.S1 library is a subtracted library derived from  
 a mixture of normalized libraries from ten regions of the  
 mouse brain (cerebellum, brain stems, olfactory bulbs,  
 hypothalamus, cortex, amygdala, basal ganglia, pineal  
 gland, striatum, hippocampus). the driver used for  
 subtraction consisted of a pool of 20,000 cDNA clones  
 obtained from non-normalized and normalized libraries of  
 these ten regions of the mouse brain."

BASE COUNT 115 a 115 c 103 g 154 t  
 ORIGIN

Query Match 18.1%; Score 357.6; DB 10; Length 487;  
 Best Local Similarity 85.3%; Pred. No. 7e-89;  
 Matches 399; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

QY 151 TTGATTATGATTACGGTCTCCCTGTATATAAATTTTACGCTGAAGCAAAATTTGGGGCCCAAC 210  
 Db 19 TCGATTATGTTATGTCAGCACCCCTGCCAAAATCAATGTGAACAATAATTCGGCTCAGC 78  
 QY 211 TCTGCTCGCTCTACTCGCTGGTGTTCATCTTTTGGTTTGTGGGCAACATGCTGGTCG 270  
 Db 79 TCTGCTCGCTCTACTCGCTGGTGTTCATCTTTTGGTTTGTGGGTAACATGATGTCT 138  
 QY 271 TCTCATCTATATAAAGCTGCAAAAAGCTGAAGTGTCTGACTGACATTTACCTGCTCAACC 330  
 Db 139 TCTCATCTATATAAAGCTGCAAAAAGCTGAAGTGTCTGACTGATATCTACTGCTCAACC 198  
 QY 331 TGCCCATCTGATCTGCTTTTCTTATTAATCTCCCATTTGGGGTCTACTCTGCTGCAA 390  
 Db 199 TGCCCATCTGATCTGCTTTTCTTATTAATCTCCCATTTGGGGTCTACTCTGCTGCAA 258  
 QY 391 ATGAGTGGGTCTTTGGGAATGCAATGTGCAAAATTTTACAGAGGCTGTATCATCGGTT 450  
 Db 259 ATGAGTGGGTCTTTGGGAATGCAATGTGTAAGTATTTACAGAGGCTGTATCATCGGTT 318  
 QY 451 ATTTTGGGGAATCTTCTCATCATCTCCTGCAACAATCGATAGATCTGGCTATTGCTCC 510  
 Db 319 ATTTTGGGGAATCTTCTCATCATCTCCTGCAACAATGTAGTACTTGGCTATTGCTCC 378  
 QY 511 ATGCTGTGTTGCTTTTAAAGCCAGGAGCTGCTTGGGGTGGTGACAAAGTGTGTATCA 570  
 Db 379 ATGCTGTGTTGCTTTTAAAGTCAAGAGCTGCTTGGGGTGGTGATAAAGTGTGTATCA 438  
 QY 571 CTGCTGTGTTGCTTTTGGTCTCTCTCCAGGAATCATCTTTTACTA 618  
 Db 439 CTGCTGTGTTGCTTTTGGTCTCTCTCCAGGAATCATCTTTTACTA 486

RESULT 4  
 AA547303  
 LOCUS  
 DEFINITION vk28h04.r1 Soares\_mammary\_gland\_NbMMG Mus musculus cDNA clone  
 IMAGE:947959 5', similar to SW:CKR2.HUMAN P41597 MONOCYTE  
 CHEMOATTRACTANT PROTEIN 1 RECEPTOR ;, mRNA sequence.  
 ACCESSION AA547303  
 VERSION AA547303.1 GI:2308594  
 KEYWORDS EST.  
 SOURCE house mouse.  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 542)  
 Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,  
 Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,  
 Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,  
 Theising,B., Wylie,T., Lennon,G., Soares,B., Willson,R. and  
 Waterston,R.  
 The WashU-HMMI Mouse EST Project  
 Unpublished (1996)  
 Contact: Marra M/Mouse EST Project  
 WashU-HMMI Mouse EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: mouseest@watson.wustl.edu  
 This clone is available royalty-free through LLNL ; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.  
 MGI:544815  
 High quality sequence stop: 286.  
 Location/Qualifiers  
 1. .542  
 /organism="Mus musculus"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:947959"  
 /clone\_lib="Soares\_mammary\_gland\_NbMMG"  
 /sex="male"

1. The first step in the process of creating a new product is to identify a market need. This involves conducting market research to understand what consumers want and what problems they are facing. Once a need is identified, the next step is to develop a concept for a product that addresses that need. This often involves brainstorming and sketching out ideas. The third step is to create a prototype, which is a preliminary model of the product. This allows the creator to test the product and make improvements before moving forward. The fourth step is to conduct a feasibility study, which involves assessing the technical, financial, and market viability of the product. Finally, the fifth step is to develop a business plan, which outlines the strategy for launching and marketing the product, as well as the financial projections for the business.

[illegible]



Db 151 CTCTCAGTGTCTTCCGAAAACACATGCTCAACGCTTTTGCAACGGTGTCAATTTTC 92

QY 1086 TACAGGGAGACAGTGGAGTACTTCAACAAACAGCCCTTCCACCTGGGGAGGAGAA 1145

Db 91 CAGCAAGACAACTCTGATCGTGCAGAGCTCAGTCTATACCGATCCACAGGAGACATGAA 32

QY 1146 GTCTCGGCTGGTTTATAAAA 1165

Db 31 GTTCTACTGGTTTAAAAA 12

RESULT 9

AL552677 907 bp mRNA linear EST 16-FEB-2001

LOCUS

DEFINITION AL552677 LTI\_NFL006.PL2 Homo sapiens cDNA clone CS0D1067YK08 5 prime, mRNA sequence.

ACCESSION AL552677

VERSION AL552677.1 GI:12891808

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 907)

Li,W.B., Gruber,C., Jesse,J. and Polayes,D.

Full-length cDNA libraries and normalization

Unpublished (2001)

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

Location/Qualifiers

1..907

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="CS0D1067YK08"

/clone\_lib="LTI\_NFL006.PL2"

/tissue\_type="placenta"

/note="Vector: pCMVSPORT 6; Site\_1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"

BASE COUNT 189 a 238 c 212 g 267 t 1 others

ORIGIN

Query Match 14.0%; Score 276.6; DB 9; Length 907;

Best Local Similarity 61.4%; Pred. No. 4.3e-66;

Matches 504; Conservative 0; Mismatches 299; Indels 18; Gaps 3;

QY 265 TGTCTCTCTCATCTTAATAACTGCAAAAGCTGAAGTCTGACTGACATTACTCTGC 324

Db 1 TGTGTCTCTCTGCTTGTGCAATACAGAGGCTAAACATGACGACATCTACTCTC 60

QY 325 TCAACTGGCCATCTCTGATCTCTTTCTTATTTACTCTCCCATTTGGGGCTCACTCTG 384

Db 61 TGAACCTGGCCATTTCTGACCTCTCTCTCTGTTCCAGCTTCCCTTGGAGTACTACA 120

QY 385 CTCGAA---ATGAGTGGGTCTTTGGGAATGCAATGCAATATTATTCACAGGCTGTATC 441

Db 121 AGTTGAAGGATGACTGGGTTTTGGTGTATGCCATGTGAAGATCTCTCTGGGTTTTATT 180

QY 442 ACATCGGTTATTTGGGGGATCTTCTTCATCATCTCTCCCTGCAATCGATAGATACCTGG 501

Db 181 ACACAGGCTTTGACAGCGAGATCTTTTTCATCATCTCTGCTGACGATTCACAGGTACTCTG 240

QY 502 CTATTGTCCATGCTGTGTTTGTCTTTAAAGCCAGGAGGCTCACCTTTGGGGTGGTGACAA 561

Db 241 CCATCGTCCACGCCGTGTTTGCTTCCGGGACGGACCGCTCACTTTTGGTGTATCACCA 300

QY 562 GTGTGATCACCCGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 621

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QY 730 TCATGCTCATCTGCTACTCGGGAATCCTGAAACCTGCTTTCGCTGCTGGAACGAGAA 789

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QY 850 CTCCCTATAACATTTGCTATCTCTCTGAACACCTTCCAGGAATTTTCGGCCTGAGTAACT 909

Db 598 CCCCTTACAATTTGACTATATCTTATTTCTGTTTCCAAAGACTTCTCTGTTTCAACCATGAGT 657

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RESULT 10

LOCUS BG205056 789 bp mRNA linear EST 21-APR-2001

DEFINITION RST24475 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.

ACCESSION BG205056

VERSION BG205056.1 GI:13726743

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 789)

Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R., Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Booser,S., Mays,R., Smith,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K., Offenbacher,J., Danzig,J. and Ducar,M.

Creation of genome-wide protein expression libraries using random activation of gene expression

Nat. Biotechnol. 19 (5), 440-445 (2001)

2127151

Contact: Scott J. Cain

Athersys, Inc.

3201 Carnegie Ave, Cleveland, OH 44115, USA

Tel: 216 431 9900

Fax: 216 361 9596

Email: scai@atersys.com

High quality sequence stop: 521.

Location/Qualifiers

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/clone\_lib="Athersys RAGE Library"

/cell\_line="HT1080"









Oncology Research  
University Health Network  
610 University Ave., 5-126, Toronto, Ontario, M5G 2M9, Canada  
Tel: (416) 946-4639  
Fax: (416) 946-6546  
Email: k.stewart@utoronto.ca  
PCR Primers  
FORWARD: 5'-GCCAAGCTCGAAATTAACCCCTCACTAAAGGG-3'  
BACKWARD: 5'-CCAGTGAATGTAATAGCACTCACTATAGGCG-3'  
Seq primer: 5'-GAAATTAACCTCACTAAGG-3'

## FEATURES

Location/Qualifiers  
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/tissue\_type="Blood"  
/cell\_type="myeloma"  
/dev\_stage="Plasma cell leukemia"  
/note="Vector: Lambda Zap Express; Site\_1: EcoRI; Site\_2: XhoI; mRNA was purified from plasma cell leukemia patient's peripheral blood containing >95% myeloma. An oligo d(T)18 primer containing XhoI restriction site was used to prime first strand synthesis using M-MLV reverse transcriptase. To protect the cDNAs from XhoI digestion in subsequent cloning step, the nucleotide analogue 5-methyl-dCTP was added to the nucleotide mixture and [a-32P]dATP was added to monitor the quantity and quality of first strand synthesis. After second-strand synthesis and blunting of cDNA termini, EcoRI adapters were ligated, followed by kinase treatment and digestion with XhoI. The cDNAs were then size-fractionated using Sephacryl S-500 column and then ligated into EcoRI and XhoI digested Lambda Zap Express vector. The ligation product was packaged using Gigapack II packaging extract. The library had primary titre of approx. 1x10<sup>6</sup>. Clones from the primary library were randomly selected for single pass sequencing."

BASE COUNT 67 a 53 c 45 g 65 t  
ORIGIN

Query Match 11.6%; Score 230; DB 12; Length 230;  
Best Local Similarity 100.0%; Pred. No. 3e-53;  
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1306 GTCACCCCAATGCATATCCACATGTCCTCAGGGAATAATCCAGAAAAAAGCTGTGGGTAGAG 1365  
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Db 1 GTCACCCCAATGCATATCCACATGTCCTCAGGGAATAATCCAGAAAAAAGCTGTGGGTAGAG 60  
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QY 1366 ACTTTTGACTCTCCAGAAAGCTCATCTCAGCTCCTGAAAAATGCCTCATTACCTTGTGCTA 1425  
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Db 61 ACTTTTGACTCTCCAGAAAGCTCATCTCAGCTCCTGAAAAATGCCTCATTACCTTGTGCTA 120  
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QY 1426 ATCCCTCTTTTCTAGTCTTCAATAATTTCTTCACTCAATCTCGATTCGTCAATGTCTTTG 1485  
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